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NOTICE OF SUBSCRIPTION RATE INCREASE

Effective with the 1996 volume, the subscription rate will be \$15 domestic and \$20 foreign. Checks or money orders in U.S. dollars should be made out to: California Fish and Game and sent to: Editors, California Department of Fish and Game, 4001 N. Wilson Way, Stockton, CA 95205.

CHANGE OF EDITORSHIP

With this issue, David W. Kohlhorst and James J. Orsi, both Senior Biologists with the Bay-Delta and Special Water Projects Division, assume the duties of Co-Editors-in-Chief of *California Fish and Game*. Their assignment to the editorship follows the Department's policy of rotating the editorship among staff members representing Marine Resources, Inland Fisheries, Wildlife Management, and Bay-Delta.

Under their guidance, the Journal will continue its policy of presenting to the public and the scientific community the results of biological investigations as they relate to management programs and the conservation of California's fish and wildlife resources. They intend to maintain and enhance the excellent reputation the Journal has gained over the last 81 years.

The new editors will be ably assisted in their duties by associate editors: Walter Beer, Ralph Carpenter, and Chuck Knutson, Inland Fisheries; Don Stevens, Bay-Delta; Dan Yparraguirre and Vern Bleich, Wildlife Management; Steve Crooke, Doyle Hanan and Ron Warner, Marine Resources; Pete Phillips and Liam Davis Environmental Services.

To Dr. Eric R. Loft, Editor-in-Chief for the past 4 years, I wish to express my appreciation for a job well done. C.F. Raysbrook, Interim Director, California Department of Fish and Game.

Publication Notice

Bibliographies on Coastal Sage Scrub and Related Malacophyllous Scrublands of Other Mediterranean-Type Climates. 1994. John F. O'Leary, Sandra A. DeSimone, Dennis D. Murphy, Peter F. Brussard, Michael S. Gilpin, and Reed F. Noss. California Wildlife Conservation Bulletin No. 10, 51 pp. This is a comprehensive collection of bibliographies on various aspects of coastal sage scrub shrublands. Sections include: Conservation, Restoration and Management; Community Composition, Distribution, and Classification; Fire, Diversity, and Succession; Soils and Water Resources; and others. It is available free of charge from Cathie Vouchilas, California Department of Fish and Game, 1416 Ninth St., Sacramento, CA 95814.

MITOCHONDRIAL DNA VARIATION AMONG POPULATIONS AND SUBSPECIES OF MULE DEER IN CALIFORNIA

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Mitochondrial DNA (mtDNA) variation of mule deer, *Odocoileus hemionus*) from eastern and southern California (n=140) and western Arizona (n=4) was assessed with restriction enzymes and compared with data from other regions (Montana, Oregon, Washington, Utah, Colorado). Eight genotypes were observed, with different frequencies among populations. There is considerable genetic structure among populations ($F_{st}=0.54$) and regions ($F_{st}=0.28$), although subspecies do not have distinctive mtDNA genotypes.

INTRODUCTION

Subspecies designations of mule deer in southern California are currently based on morphology (Cowan 1936, Bowyer and Bleich 1984, Wallmo 1981). Cowan (1936) studied body and skull measurements and pelage and antler characteristics and identified five subspecies of mule deer in California: Rocky Mountain mule deer, *Odocoileus hemionus hemionus*, California mule deer, *O. h. californicus*, southern mule deer, *O. h. fuliginatus*, burro mule deer, *O. h. eremicus*, and Inyo mule deer, *O. h. inyoensis*. Additionally, Columbian black-tailed deer, *O. h. columbianus*, and Sitka black-tailed deer, *O. h. sitkensis*, occur along the Pacific coast from central California to Alaska, and desert mule deer, *O. h. crooki*, inhabit southern Arizona, New Mexico, Texas, and northern Mexico. Subspecies locations are shown in Figure 1. Other authors have suggested that some of these subspecies designations are in need of revision. Wallmo (1981) described several biologists' opinions that *inyoensis* is a questionable subspecies. Hoffmeister (1962) disposed of *eremicus* and synonymized this taxon with *crooki*, but Bowyer and Bleich (1984) thought Hoffmeister's assessment was inadequate. In addition, Bowyer and Bleich (1984) showed that clinal intergradation of morphological characters occurs between *fuliginatus* and *eremicus* in eastern San Diego County and southcentral Riverside County.

As in other taxa, there is not a consensus on subspecies designations for

O. hemionus because of inadequate quantitative analyses, small sample sizes, and the subjective nature of subspecies designations (Mayr 1963, Avise and Ball 1990, Cronin 1993). For *O. hemionus*, it is likely that more thorough analyses of morphology will show intergradation of characters and make subspecies designations difficult or inconsistent (Bowyer and Bleich 1984). This would be relatively unimportant for wildlife management except that subspecies designations are often used as the basis for endangered species listing (e.g., USFWS 1995), and formal subspecies designations suggest to the public that there is consensus among biologists regarding the taxonomy of a group. It is therefore important to carefully consider all relevant information when considering subspecies designations (Geist 1992, Cronin 1993).

Avise and Ball (1990) have recently provided a modern definition of subspecies which incorporates the concept of phylogenetic relatedness as the primary criterion for classification of subspecies. Subspecies are "groups of actually or potentially interbreeding populations phylogenetically distinguishable from, but reproductively compatible with, other such groups. Importantly, the evidence for phylogenetic distinction must normally come from the concordant distributions of multiple, independent, genetically based traits" (Avise and Ball 1990). Genetic data can be useful in taxonomy, and modern molecular genetics methods are increasingly being used for studies of subspecies (e.g., Cronin 1993).

There have been many genetic studies of *Odocoileus* (reviewed by Carr and Hughes 1993, Cronin 1991a, Smith et al. 1984), beginning with the pioneering work on serum proteins by Cowan and Johnston (1962). Cowan and Johnston compared electrophoretic mobility of serum proteins and found differences between *O. h. hemionus*, *O. h. sitkensis* and *O. h. columbianus*. However, sample sizes were small (two-five of each subspecies) and mobility differences were not absolute between subspecies. More extensive studies of allozyme variation have shown considerable allele frequency differences between subspecies and populations, including *O. h. hemionus*, *O. h. sitkensis*, and *O. h. columbianus* (Gavin and May 1988, Cronin et al. 1988, Cronin 1991a, Scribner et al. 1991). To our knowledge, allozyme data for *O. hemionus* from California are lacking.

To assess genetic variation of mule deer in California we analyzed mitochondrial DNA (mtDNA) because of the extensive mtDNA data available for *O. hemionus* from other areas (Cronin 1991a, Ballinger et al. 1992, Carr and Hughes 1993). MtDNA is a useful genetic marker for assessing population structure and phylogenetic relationships (Avise 1994). In mammals, mtDNA generally has a clonal, maternal mode of inheritance and is useful for tracing maternal lineages and female-mediated gene flow. The phylogenetic relationships of *Odocoileus* spp. are complicated by the similarity of mule deer and white-tailed deer (*O. virginianus*) mtDNA, and are described elsewhere (Carr et al. 1986, Cronin et al. 1988, Cronin 1991b, Ballinger et al. 1992, Carr and Hughes 1993). In this study, we are concerned with the relationships among subspecies and populations of only *O. hemionus*.

Previous studies have shown distinct mtDNA genotypes characteristic of mule deer, *O. h. hemionus* and *O. h. crooki*, and black-tailed deer, *O. h. columbianus* and *O. h. sitkensis* (Carr et al. 1986, Cronin et al. 1988). Allozyme studies show differentiation

of nuclear genes of mule deer and black-tailed deer as well, although molecular sequence differentiation cannot be quantified with these methods (Cronin 1991a). The nucleotide sequence divergence of the mule deer and black-tailed deer mtDNA genotypes is 6-7%, which is very high for conspecifics. In contrast, sequence divergence of variant genotypes within either the mule deer or black-tailed deer subspecies is relatively low (<1%). The black-tailed deer mtDNA genotypes occur along the Pacific Coast, west of the Sierra Nevada and Cascade Mountains from Alaska to as far south as Santa Clara County, California (Cronin 1991a, Carr and Hughes 1993). The mule deer mtDNA genotypes occur east of the Sierra Nevada and Cascade Mountains, throughout the Rocky Mountains, Great Basin, and west Texas. The mule deer mtDNA genotypes also occur west of the Sierra Nevada in Santa Clara and San Luis Obispo counties, California. As with morphology, the distribution of mtDNA genotypes in *O. hemionus* probably intergrades along the Pacific Coast from the mule deer genotypes in the south to the black-tailed deer genotypes in the north, with a zone of overlap in central California.

The mtDNA data for *O. hemionus* in California are limited to small numbers of samples north of San Luis Obispo County. Our objectives are to quantify the mtDNA genotype distributions among populations and subspecies in eastern and southern California and western Arizona. We will also compare the mtDNA of mule deer in California and Arizona with that from other locations across western North America.

METHODS

Samples (20-50 g) of skeletal muscle from mule deer killed by automobiles or hunters during 1990-1992 in California were obtained from California Department of Fish and Game (CDFG) personnel. Samples from Arizona were obtained from hunter-killed animals during the 1991 hunting season. Upon collection, tissue samples were placed in plastic bags, labeled, and frozen until analyzed. Samples were obtained from several locations in southern and eastern California and from extreme southwestern Arizona. Sampling locations within the same geographic areas or ecological zones (Transverse Ranges, Peninsular Ranges, Inyo and White Mountains) were pooled into "populations" for analyses. We also considered the following areas to represent populations: Arizona Sonoran Desert, California Sonoran Desert, and Round Valley in the eastern Sierra Nevada (Figure 1). We assigned subspecies names using geographic ranges as described by Cowan (1936), Bowyer and Bleich (1984), Hoffmeister (1962), and Wallmo (1981). Deer from the eastern Mojave Desert, California, were not assigned to a subspecies or compared with the other California/Arizona populations because they descend from animals translocated to that area from southwestern ($n = 7$) and northeastern ($n = 40$) California, and from Catalina Island ($n = 21$) during 1945-49 (Leja 1976, Longhurst et al. 1952). The deer from Catalina Island were the descendants of three animals from northeastern California and 19 from Los Angeles County, originally translocated to Catalina Island between 1928-1932 (Leja 1976). In addition to the California populations, we compared mtDNA variation among geographic "regions" using the data of Cronin (1991a). Regions were California/Arizona (all populations),

eastern Montana, western Montana, Washington, Oregon, Utah, and Colorado.

Genomic DNA was isolated from muscle tissues, and the entire mtDNA molecule was analyzed for restriction fragment polymorphisms with southern blots as described by Cronin (1991a). Four restriction enzymes (*EcoRI*, *SacI*, *HpaI*, *HaeIII*) were used on 18 deer from California and a total of 34 deer from Oregon, Washington, Colorado, and Utah. These four enzymes showed variation in mule deer from other locations (Cronin 1991b). Two of the four enzymes, *EcoRI* and *HaeIII*, revealed mtDNA variation in the California samples, and were used to analyze the entire sample of 135 deer from California and four from Arizona. These two enzymes have been used to identify genotypes in mule deer from several populations (Cronin et al. 1988, Cronin 1991a). MtDNA genotype frequencies were compared among populations and regions with estimates of F_{st} (Wright 1978), a measure of the variance of genotypes among populations. This approach, which ignores the phylogenetic relationships of the genotypes, is often employed in mtDNA studies of population structure (DeSalle et al. 1987, Cronin et al. 1991, Avise et al. 1990, Ellsworth et al. 1994).

RESULTS AND DISCUSSION

Three of the four enzymes used to analyze the 18 mule deer from California and 34 mule deer from other locations resulted in restriction fragment patterns identical to those described by Cronin (1991a,b) for mule deer across western North America. This included one pattern each for *SacI* and *HpaI*, and two patterns for *EcoRI* (Table 1). Eight fragment patterns, including unique fragment patterns for some California and Arizona deer, were obtained with *HaeIII*. *HaeIII* patterns 10, 11, and 3L were not observed in earlier studies and occurred only in California and Arizona deer. Black-tailed deer have distinctive mtDNA fragment patterns (Cronin et al. 1988) that were not observed in any of our California/Arizona samples. The mule deer we examined from southern California and Arizona have mtDNA genotype which are similar to those of mule deer across western North America (Cronin 1991a).

Although all mule deer have similar mtDNA, variant genotypes can be defined by the variable restriction fragment patterns resulting from analyses with *EcoRI* and *HaeIII*. Genotypes are defined as the combination of the fragment patterns for the two enzymes (Table 2). For example, a deer that has *EcoRI* fragment pattern 1 and *HaeIII* fragment pattern 3 has genotype D.

The eight mtDNA genotypes vary in frequency among the six California and Arizona populations (Figure 1, Table 3) and there is a high level of population subdivision ($F_{st}=0.541$). Genotype A is most common in the Transverse and Peninsular range populations. Genotype A is also common in the translocated mule deer in the eastern Mojave Desert. Genotype D predominates in California's Sonoran Desert, and genotype L in the Arizona Sonoran Desert. Genotype B occurs mostTable 1. Mitochondrial DNA restriction fragment Table 1. Mitochondrial DNA restriction fragment patterns in mule deer. Numbers refer to size of fragments (kilobases).

Table 1. Mitochondrial DNA restriction fragment patterns in mule deer. Numbers refer to size of fragments (kilobases).

Restriction Enzyme	Fragment Pattern							
	1	2	3	3L	6	7	10	11
<i>EcoRI</i>	8.9	8.9						
	3.1	3.6						
	1.9	3.1						
	1.7	0.9						
	0.9							
<i>HpaI</i>	7.8							
	3.7							
	3.4							
	1.7							
<i>SacI</i>	10.7							
	3.2							
	2.7							
<i>HaeII</i>	4.0	4.0	4.0	4.5	3.0	2.7	4.0	4.0
	1.1	2.6	1.3	1.3	1.3	1.1	1.8	2.6
	1.0	1.2	1.1	1.1	1.1	1.0	1.1	1.1
	0.8		1.0	1.0	1.0	0.8	1.0	1.0
								0.8

Table 2. mtDNA genotypes as defined by restriction fragment patterns in mule deer. Descriptions of the fragment patterns are in Table 1.

Genotype	Restriction Fragment Pattern	
	<i>EcoRI</i>	<i>HaeIII</i>
A	1	1
B	2	2
D	1	3
E	1	6
F	1	7
K	1	10
N	2	1
O	1	3L
L	1	11
M	2	11

frequently in deer wintering in Round Valley in the eastern Sierra Nevada Mountains. Genotype K occurs most frequently in deer from the Inyo and White mountains of eastern California. Rare genotypes appear to be limited in distribution, although our sample sizes are not large enough for these results to be definitive. For example, genotypes N and K are restricted to the Inyo/White mountains population and L is restricted to the Transverse range, Peninsular range, Arizona Sonoran Desert and the translocated Mojave Desert populations. Genotype M is restricted to the Peninsular

Table 3. Mule deer sample sizes (n) and mtDNA genotype frequencies of seven California and Arizona populations, and six other locations* as reported by Cronin (1991a). For the Transverse Ranges, Peninsula Ranges, and Inyo/White Mountains populations, the numbers of deer with each genotype for each sampling location are given in parentheses.

each sampling location are given in parentheses.												
			MIDNA GENOTYPES									
SUBSPECIES	REGION	n	A	B	D	K	L	M	N	O	E	F
California/Arizona Region												
	Population (sampling location)											
<i>crooki</i>	Arizona Sonoran Desert	4	-	-	0.25	-	0.75	-	-	-	-	-
<i>eremicus</i>	California Sonoran Desert	35	-	-	0.80	-	-	0.03	-	0.17	-	-
<i>californicus</i>	Transverse Ranges	32	0.97	-	-	-	0.03	-	-	-	-	-
	(Santa Ynez Mountains)		(18)	-	-	-	-	-	-	-	-	-
	(San Gabriel Mountains)		(5)	-	-	-	-	-	-	-	-	-
	(San Bernadino Mountains)		(8)	-	-	-	(1)	-	-	-	-	-
<i>fuliginatus</i>	Peninsular Ranges	22	0.91	-	-	-	0.05	0.05	-	-	-	-
	(San Jacinto Mountains)		(9)	-	-	-	-	-	-	-	-	-
	(Laguna/Cuyamaca Mountains)		(11)	-	-	-	(1)	(1)	-	-	-	-
<i>inyoensis</i>	Round Valley	11	0.18	0.82	-	-	-	-	-	-	-	-
<i>inyoensis</i>	Inyo/White Mountains	21	0.19	0.29	-	0.38	-	-	0.14	-	-	-
	(Inyo Mountains)		(1)	(2)	-	(3)	-	-	(3)	-	-	-
	(White Mountains)		(3)	(4)	-	(5)	-	-	-	-	-	-
undefined	Eastern Mojave Desert	14	0.79	-	-	-	0.21	-	-	-	-	-
<i>*hemionus</i>	Montana-East Region	1700.20	0.68	0.12	-	-	-	-	-	-	-	-
<i>*hemionus</i>	Montana-West Region	55 0.24	0.02	0.74	-	-	-	-	-	-	-	-
<i>*hemionus</i>	Colorado Region	68	0.48	0.25	0.23	-	-	-	-	-	0.01	0.01
<i>*hemionus</i>	Utah Region	23	0.96	-	0.04	-	-	-	-	-	-	-
<i>*hemionus</i>	Oregon Region	220.27	0.27	0.45	-	-	-	-	-	-	-	-
<i>*hemionus</i>	Washington Region	9 -	0.78	0.22	-	-	-	-	-	-	-	-

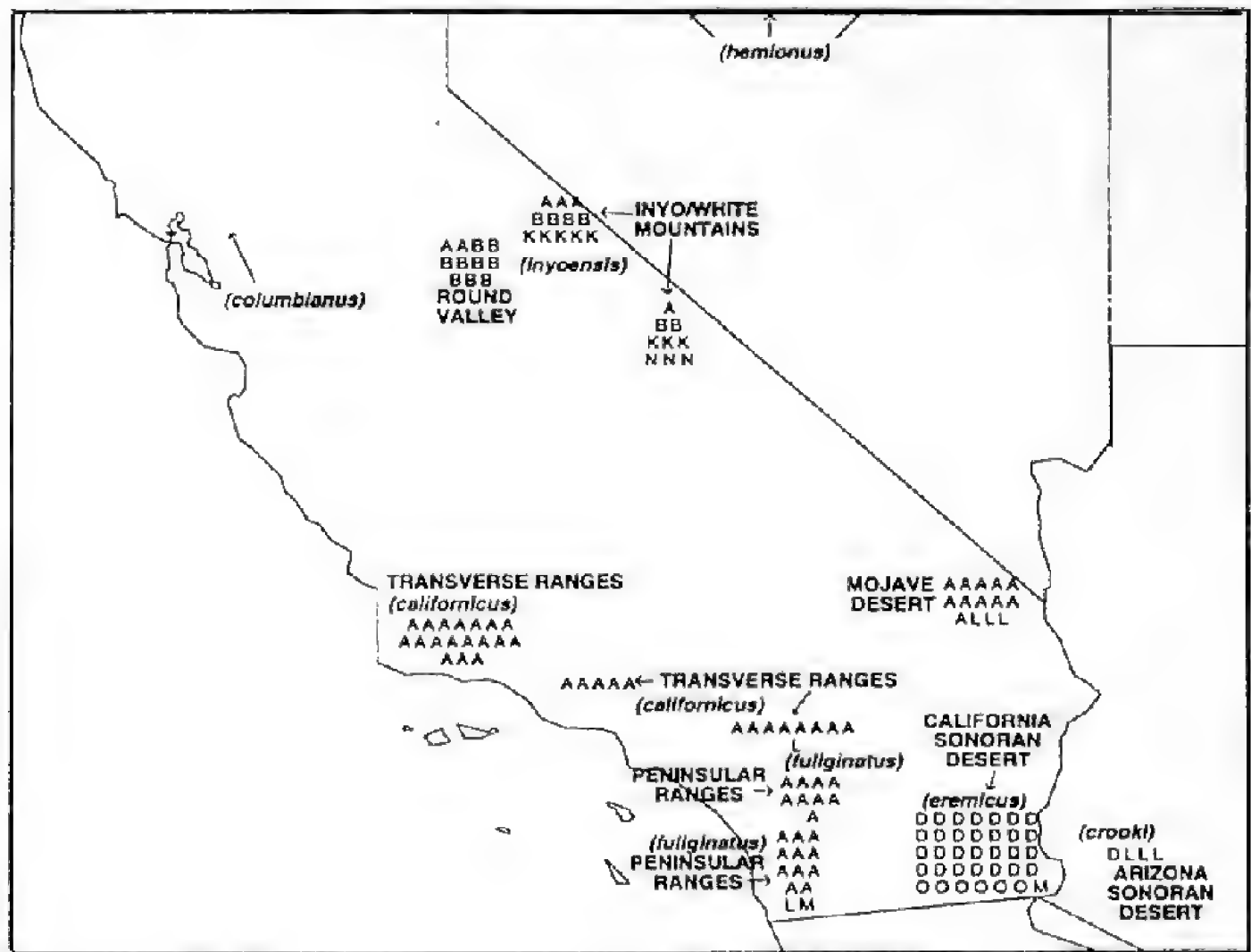


Figure 1. Distribution of mule deer mtDNA genotypes among sampling locations in California. Each small letter represents a deer with a genotype as described in Table 1. Subspecies names are in parentheses.

and California Sonoran Desert populations, and O to the California Sonoran Desert population.

The predominance of genotype A in the Peninsular and Transverse Range populations, genotype B in the Inyo/White Mountains and Round Valley populations, and genotype D in the Arizona and California Sonoran Desert populations suggests these pairs of populations may represent subregional groups within the California/Arizona region. A considerable level of differentiation ($F_{st} = 0.455$) is apparent if these three pairs of populations are combined into three subregions. Further investigations are warranted to quantify subregional differentiation.

For comparison across the range of *O. hemionus*, we have included the mtDNA genotypes from other regions (Table 3). The common genotypes in California (A, B, D) occur across western North America. As in California, these genotypes vary in frequency among populations. For example, the frequency of genotype B, which in California occurs only in the Round Valley and Inyo/White Mountains populations, varies from 0.78 in Washington to 0.02 in western Montana. Likewise, genotype D is common in Montana, Colorado, Washington, Oregon, and the California Sonoran Desert population, but absent in the other California populations, and rare in Utah. In

addition to the common genotypes, several genotypes (K, L, M, N, and O) are restricted to California and Arizona. This indicates a degree of differentiation of California/Arizona from the other geographic regions. The variance of genotype frequencies among all regions ($F_{st} = 0.284$) shows a high degree of genetic differentiation, although lower than that among populations and subregions in California and Arizona.

There is considerable differentiation of mtDNA genotype frequencies among populations and groups of populations (subregions) within the California/Arizona region and among other geographic regions. The level of mtDNA differentiation ($F_{st} = 0.2-0.6$) is similar to that for other deer populations (Cronin et al. 1991, Ellsworth et al. 1994, Cronin 1991a). This has probably resulted from different colonization histories followed by restricted gene flow (Slatkin 1987, Wade and McCauley 1988). Founder effects and genetic drift may have resulted in the high variance in frequencies of genotypes among populations and regions. We emphasize that mtDNA genotype distribution will reflect female-mediated gene flow, as mtDNA is maternally inherited. Biparentally-inherited genetic markers may help quantify the contribution of both sexes to gene flow (Cronin et al. 1991, Ellsworth et al. 1994).

Although there is mtDNA differentiation among *populations and regions*, the morphologically-defined *subspecies* in California do not have unique mtDNA genotypes. The same mtDNA genotypes in *O. h. crooki*, *O. h. californicus*, *O. h. eremicus*, *O. h. fuliginatus*, and *O. h. inyoensis* also occur in *O. h. hemionus* across western North America (Table 3). As the data in Table 3 indicate, there is genetic differentiation of populations and regions, but it is not strictly associated with geographic distance or subspecific designation. The mule deer subspecies, as currently defined, are not identifiable as phylogenetically distinct with the mtDNA data. However, the possible subregional differentiation of mtDNA genotype frequencies (Fig. 1) suggests a close genetic relationship of *O. h. eremicus* and *O. h. crooki* in the Sonoran Desert (as suggested by Hoffmeister 1962), and *O. h. californicus* and *O. h. fuliginatus* in the Transverse/Peninsular Ranges.

As with many other highly mobile large mammals, there is considerable population genetic structure in mule deer, but morphologically-defined subspecies do not have distinctive mtDNA (Cronin 1993). A notable exception is the highly divergent mtDNA of all the mule deer subspecies and the two black-tailed deer subspecies (Carr et al. 1986, Cronin et al. 1988). The morphological variation among these groups may result from environmental (non-genetic) effects, strong natural selection, genetic drift within populations, or a combination of these factors. The clinal variation in morphology of *O. hemionus* along the Pacific coast suggests selection pressures are at work (Cowan 1936, Wallmo 1981), but this is difficult to verify (Endler 1977). More intensive studies of nuclear genetic markers and basic ecology are needed to understand the intraspecific systematic relationships of *O. hemionus*. Such studies may be useful in identifying populations as units for

management and conservation.

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USING SPOTLIGHT COUNTS TO ESTIMATE MULE DEER POPULATION SIZE AND TRENDS

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In the past, population size of the North Kings herd of mule deer, *Odocoileus hemionus*, in California has been estimated from the number of adult males killed during hunting season. This method is inaccurate and yields no measure of precision. We examined the use of spotlight transects conducted during summer, both with and without the measurement of perpendicular distances, to answer: 1) can the numbers of deer seen along standardized spotlight routes be used as an index to changes in deer numbers, 2) can the additional estimation of perpendicular distances be used to derive deer densities using line transect theory, and 3) can deer densities be applied to the entire summer range of the North Kings deer herd to estimate total population size? Fawns were not accurately represented in spotlight counts because of their small size and secretive behavior. Number of adult deer seen per km of transect was influenced by transect and observer. Despite consistent training, some observers were better at seeing deer than others. There did not appear to be yearly differences in number of deer seen, but observer effects were confounded with year effects. In most cases, fewer deer were seen within 18 m of the road than in the next interval (19-37 m), but deer did not move away from the center of the transect in response to the presence of observers. Because deer appeared to avoid roads, deer densities based on road transects could not be used to reliably estimate total herd size.

INTRODUCTION

The North Kings mule deer, *Odocoileus hemionus*, herd is located in the Sierra Nevada northeast of Fresno, California (Fig. 1). This migratory herd was estimated at 17,000 animals in 1950, 3,500 animals in 1972, and only 2,000 animals in 1986 (Bertram 1984, Neal et al. 1987). Because of the decline, the herd has been the focus of numerous habitat improvement projects (Chapel and Rempel 1981, Bertram 1984). Cause of the decline is unknown, but it has been suggested that heavy predation by mountain lions, *Felis concolor*, has prevented the herd from responding to habitat improvement (Neal et al. 1987). However, the technique used to estimate deer population size in the North Kings herd (Dasmann 1952, Bertram 1984) lacks sufficient power to detect the relatively small changes in deer numbers expected under even extensive habitat improvement

work (Verner and Kie 1988).

Dasmann (1952) outlined two methods for estimating deer population sizes based on harvest information: 1) using harvest data in combination with pre- and post-hunt sex and age ratios, and 2) using the harvest data alone. Dasmann (1952:231) provided tables for use when adequate pre- and post-season sex and age ratios were not available. These tabular values have been used to estimate deer numbers in the North Kings herd (Bertram 1984). However, by using the tabular values "a relatively constant hunting pressure is assumed, as well as relatively constant ratios, hence use of a single year's data may give misleading results" (Dasmann 1952:232). We believed that spotlight counts made along fixed road transects might provide either an index to changes in deer numbers, or actual estimates of deer densities that were more precise than the method currently in use (Kie 1988).

Spotlight counts have been conducted on the George Reserve in Michigan with a population of white-tailed deer, *O. virginianus*, of known size and composition (McCullough 1982). Sex and age ratios differed between months, with buck:doe ratios closely approximating true values in July, and fawn:doe ratios being most accurate in April when the fawns were almost 10 months old.

Spotlight counts have also been used to estimate densities of white-tailed deer in south Texas (Fafarman and DeYoung 1986). The area being counted was estimated by measuring the distance from the center of their transect line to where deer were no longer visible because of screening cover. Deer density estimates were then compared to those obtained from helicopter counts. Assuming helicopter counts represented 65% of the true population density (DeYoung 1985), spotlight counts revealed between 80% and 98% of the true density.

Black-tailed deer, *O. h. columbianus*, in western Oregon have also been counted using spotlight methods (Dealy 1966). Between 65 and 80% of all deer seen were first observed while standing upright rather than lying down. It was suggested that the ratio of standing to lying deer could affect the number of deer counted.

Trends in black-tailed deer numbers on Vancouver Island in British Columbia have been estimated using spotlight counts (Harestad and Jones 1981). Counts differed between different seasons of the year. Within a single season, the coefficient of variation of separate counts declined rapidly at first with increasing mean numbers of deer counted, and stabilized after a mean count of 50-100 deer.

Spotlight counts have also been compared with daylight counts for determining sex and age ratios in black-tailed deer in northern California (McCullough 1993). Although spotlight counts were less biased than daylight counts, variations suggested biases of unknown origin that could not be corrected by replication.

In all but two of the studies just mentioned, no attempt was made to estimate or measure the area being counted. McCullough (1982) and Fafarman and DeYoung (1986) surveyed the census routes they used to derive a measure of the total area being sampled, and used that area as a basis to estimate deer density. An alternative method makes use of line transect theory.

Line transect counts consist of an observer traversing a route of known length, counting the number of animal seen, and recording their perpendicular distances to the

center of the transect line (Buckland et al. 1993). We explored the possibility of using spotlight counts on summer range as an alternative method for monitoring changes in the size of the North Kings deer herd. We specifically addressed the following: 1) can the numbers of deer seen along standardized spotlight routes be used as an index to changes in deer numbers, 2) can the additional estimation of perpendicular distances be used to derive deer densities using line transect theory, and 3) can deer densities be applied to the entire summer range of the North Kings deer herd to estimate total population size?

STUDY AREA

The study was conducted on the summer range of the North Kings deer herd (Fig. 1). Seasonal ranges for the herd occur from 300 m elevation along the Kings River (winter range) to over 3,900 m along the Sierra Crest to the northeast (summer range). We limited most of our study to the western half of the summer range (Dinkey segment) (Chapel and Rempel 1981), between 1,750 and 2,700 m elevation. The eastern half (Crown segment), located mostly within wilderness areas, was not accessible by motor vehicle. Habitat types on the study area included ponderosa pine, Sierran mixed conifer, white fir, red fir, lodgepole pine, subalpine conifer, montane chaparral, and montane riparian (Mayer and Laudenslayer 1988).

METHODS

We established six spotlight transects on improved dirt roads in the study area (Fig. 1, Table 1). These transects were located in areas where deer were known to be common during summer. Three transects were sampled nightly for 4 nights each week from late June through early September in 1989, 1991, and 1992. Transects were begun 1-h after sunset.

Direction of travel on the transect was alternated each time it was sampled. On the three transects with only one outlet (Cabin Meadow, Smith Meadow, and Hoffman Mountain) this procedure required traveling the length of the transect on alternate nights before starting. When this was necessary, the observers remained at the starting point for 30 min to minimize the effects of disturbance along the transect. There was no significant effect of direction of travel on the numbers of deer seen on those three transects ($P > 0.10$).

Seven observers took part in sampling during the 3-year study. Each was trained in sampling protocol, detecting deer, and estimating distances before collecting data. Usual procedure involved one person driving a pickup truck at ≤ 16 km/h with a single observer standing in back using a 1 X 10⁶ candle-power spotlight. When deer were detected, the truck was stopped and the observer estimated the perpendicular distance from the center of the transect to the deer or center of the group of deer. Distances were estimated to the nearest 4.6 m (5yds). Each deer was recorded as standing or bedded, adult or fawn, and if adult, male or female.

Two observers were occasionally used in the back of the truck. Also on occasion,

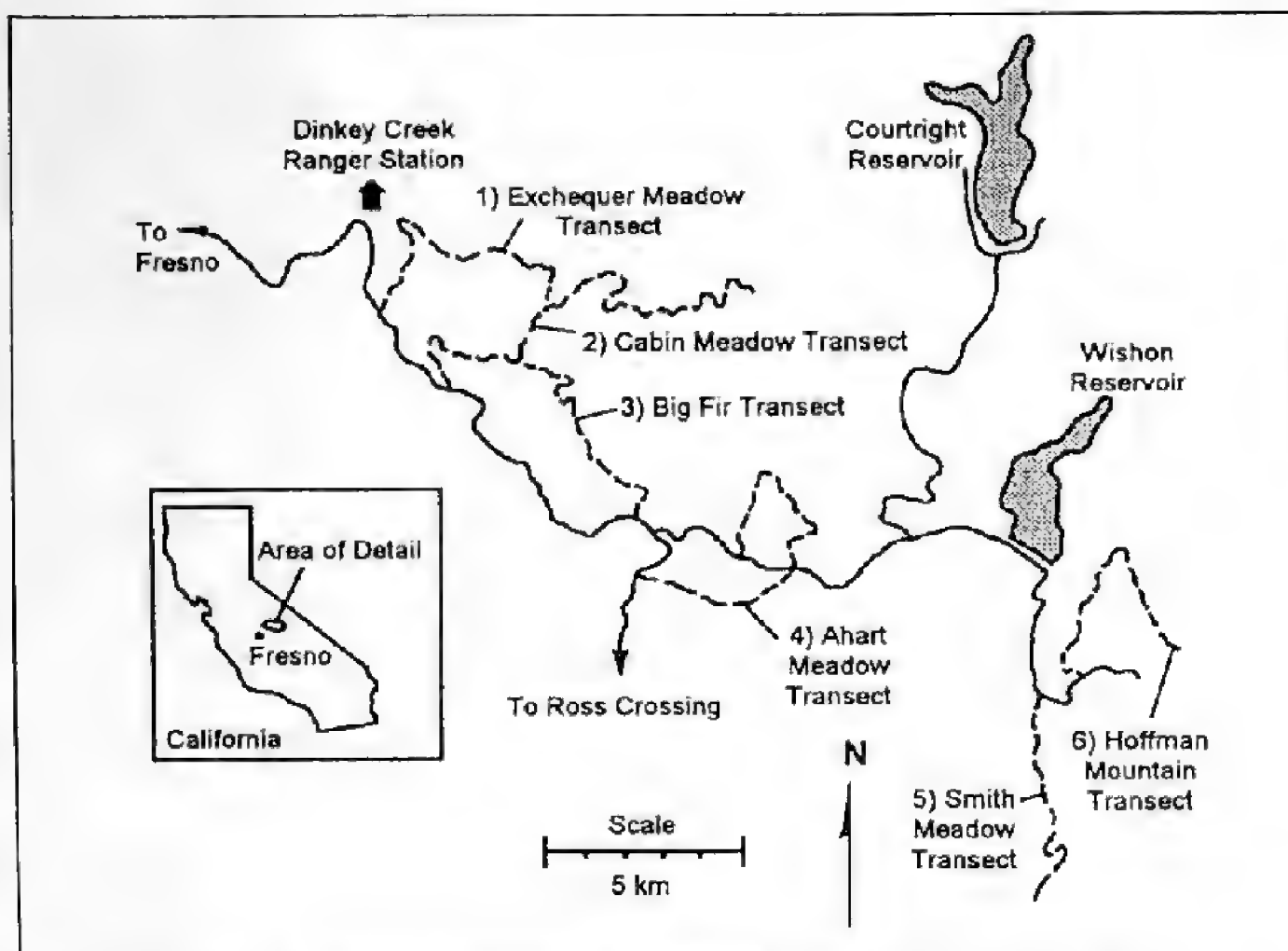


Figure. 1. Location of the six numbered spotlight-count transects in central California.

especially in the first year of the study, miscellaneous other observers including supervisory personnel were used. These changes in protocol were recorded and the effects examined.

We performed preliminary data analysis by considering only the number of adult deer and fawns seen during each transect run, while ignoring the perpendicular distance information. To eliminate the effect of differing transect lengths, we expressed numbers of deer seen in each class on a per km basis. Standard analysis of variance or covariance techniques are not appropriate for experimental designs with empty cells such as ours. Therefore we used a general linear model (GLM) approach (Minitab 1991).

For the analysis of deer seen per km of transect, the sampling unit was defined as a single run on one of the transects. The GLM main factors included: year (three levels), semi-monthly period (eight levels, from early June through late September), observer (nine levels), and transect (six levels). We also included year x transect and period x transect interactions, and days to the nearest full moon (as a measure of moonlight present) as a covariate. We also used GLMs to examine sex and age ratios of deer seen (bucks per 100 does and fawns per 100 does).

To estimate actual deer densities, we analyzed the perpendicular distances to each group of deer using program DISTANCE (Laake et al. 1994). Line transect analysis assumes: 1) groups of deer directly on the center of the transect are always detected, 2) groups of deer are detected at their initial location prior to any movement resulting

Table 1. Transect lengths, number of transects driven, groups of deer seen, mean, and standard deviation of adult deer and fawns seen per km of transect on each run.

Transect and Year	Number of Runs	Groups Seen	Fawns Seen Per Km		Adults Seen Per Km	
			Mean	(SD)	Mean	(SD)
Exchequer Meadow (9.5 km)						
1989	24	139	0.623	(0.301)	0.228	(0.166)
1991	19	88	0.527	(0.248)	0.155	(0.158)
1992	24	118	0.571	(0.278)	0.149	(0.189)
All Years	67	345	0.577	(0.277)	0.179	(0.174)
Cabin Meadow (16.4 km)						
1989	24	113	0.328	(0.222)	0.074	(0.112)
1991	19	129	0.481	(0.242)	0.131	(0.124)
1992	25	119	0.300	(0.141)	0.093	(0.098)
All Years	68	361	0.360	(0.214)	0.097	(0.112)
Big Fir (7.9 km)						
1989	24	73	0.407	(0.277)	0.090	(0.102)
1991	19	55	0.401	(0.258)	0.087	(0.141)
1992	10	31	0.431	(0.312)	0.051	(0.123)
All Years	53	159	0.409	(0.272)	0.081	(0.120)
Ahart Meadow (13.0 km)						
1989	20	98	0.441	(0.202)	0.035	(0.046)
1991	18	59	0.247	(0.143)	0.081	(0.169)
1992	24	98	0.297	(0.196)	0.080	(0.125)
All Years	62	255	0.329	(0.199)	0.066	(0.123)
Smith Meadow (9.0 km)						
1989	21	43	0.190	(0.117)	0.021	(0.045)
1991	19	35	0.187	(0.166)	0.018	(0.076)
1992	23	66	0.309	(0.244)	0.077	(0.136)
All Years	63	144	0.233	(0.192)	0.041	(0.098)
Hoffman Mountain (9.7 km)						
1989	22	160	0.848	(0.367)	0.174	(0.121)
1991	19	88	0.562	(0.257)	0.076	(0.076)
1992	24	110	0.587	(0.292)	0.099	(0.157)
All Years	65	358	0.668	(0.332)	0.118	(0.131)

from the presence of the observers, and 3) distances are measured accurately (Buckland et al. 1993).

In our study, deer standing in the middle of the road were always detected, satisfying the first assumption. Violation of the second assumption is not uncommon in line transect sampling as animals may move away from the center of the transect before being detected. This can result in animals being seen more frequently in intermediate distance intervals than in those intervals adjacent to the center of the transect. In many cases, evasive movement cannot be detected from the data alone (Buckland et al. 1993). A natural reluctance to use areas immediately adjacent to the

road (Rost and Bailey 1979) could result in the same pattern in the data even in the absence of observers.

We hypothesized that if deer were moving away from the center of the transect as a result of our presence before they were detected, then the percentage of deer seen standing (versus bedded) would decrease as a function of distance away from the road. If the hypothesis were true, deer bedded close to the road would have been more likely to stand and begin moving away than would deer bedded at some distance away. We tested this hypothesis.

The third assumption is that distances from the center of the transect to each group of deer are measured accurately. To help satisfy this assumption, we truncated our data at 91 m (100 yds) to avoid the uncertainties associated with estimating long distances. To avoid the problem of data heaping which occurs when observers use even distance intervals more often than odd intervals, we grouped our data recorded by 4.6 m intervals into 18 m (20 yd) groups (Laake et al. 1994).

We used groups of deer as objects rather than individual deer, even though most groups consisted of a single deer (Buckland et al. 1993). Program DISTANCE tests for differential visibility of clusters (larger groups of deer being more visible at long distances than smaller groups) by regressing the natural log of cluster size against the detection function $g(x)$. If the regression was significant ($P < 0.05$), size-biased estimates of cluster sizes were used to estimate deer densities. Otherwise mean cluster size was used (Buckland et al. 1993, Laake et al. 1994).

To estimate deer densities, we combined all the data from a single transect in a single year rather than treating each separate transect run as a replicate as we did in the previous analysis (Buckland et al. 1993). Total transect length then became the length of each transect multiplied by the number of times that transect was run each year.

Program DISTANCE fitted several robust models to the frequency-distance data, first without and then with modifications (Laake et al. 1994). It chose a parsimonious model that was neither underfit (too few parameters resulting in model bias) nor overfit (too many parameters resulting in unnecessarily large variances) on the basis of Akaike's Information Criterion (Akaike 1973, Buckland et al. 1993, Laake et al. 1994). DISTANCE then estimated cluster (group) and individual deer densities for each transect separately and for all the transects in a given year combined. We report only the estimated densities for individual deer. Asymmetrical 95% confidence intervals were calculated using degrees of freedom obtained by the method of Satterthwaite (1946, see Buckland et al. 1993, Laake et al. 1994 for details).

RESULTS

Factors Affecting Deer Seen on Transects

A total of 378 runs (one run represented a single transect driven on a single night) were made on the transects during the 3-year study, and 1,622 groups of deer were seen (Table 1). Number of deer seen during each run was highly variable between transects and between years within transects (Table 1). Among all adult deer seen, 72% were first seen standing versus bedded (adult females = 72%, adult males = 71%), while among fawns, only 36% were first seen standing.

Table 2. Summary of multiple-factor general linear model (GLM) F values for adult and fawn deer seen per km during each transect run.

Source	Adult Deer Seen Per Km	Fawns Seen Per Km
Year	$F_{2,309} = 1.27$ $P = 0.28$	$F_{2,309} = 1.38$ $P = 0.25$
Period	$F_{7,309} = 0.96$ $P = 0.46$	$F_{7,309} = 5.59$ $P < 0.01$
Observer	$F_{8,309} = 2.60$ $P < 0.01$	$F_{8,309} = 0.85$ $P = 0.56$
Transect	$F_{5,309} = 22.8$ $P < 0.01$	$F_{5,309} = 3.61$ $P < 0.01$
Year x Transect	$F_{10,309} = 3.55$ $P < 0.01$	$F_{10,309} = 1.99$ $P = 0.03$
Period x Transect	$F_{35,309} = 1.98$ $P < 0.01$	$F_{35,309} = 1.64$ $P = 0.02$
Days To Nearest Full Moon (Covariate)	$F_{1,309} = 1.04$ $P = 0.31$	$F_{1,309} = 0.09$ $P = 0.77$

Year did not affect either the number of adults ($P = 0.28$) or fawns ($P = 0.25$) seen per km (Table 2). Mean numbers of adult deer seen per km of transect driven were 0.47, 0.40, and 0.41 in 1989, 1991, and 1992 (Fig. 2). Numbers of fawns seen were fairly constant at 0.11, 0.09, and 0.10 per km in 1989, 1991, and 1992 (Fig. 2).

Period did not significantly affect the number of adult deer seen per km ($P = 0.46$), but it strongly influenced the number of fawns seen per km ($P < 0.01$) (Table 2). Numbers of fawns seen increased as the summer progressed and fawns became older (Fig. 3). Only 12 transect runs were made in late September (period 8) during the 3-year study, and the resulting 95% confidence interval was large (Fig. 3). Therefore, we do not know if the numbers of fawns seen had stabilized at that time.

There were significant effects of observer on adult deer seen ($P < 0.01$), but not on numbers of fawns seen ($P = 0.56$) (Table 2). Some observers were better than others at spotting adult deer (Table 3). Two observers were not significantly better ($P > 0.10$) at seeing adult deer (0.520 adult deer per km, SD = 0.326, $n = 24$ runs) (Table 3) than a single observer (0.426, SD = 0.290, $n = 354$ runs).

Observers were almost completely nested within years. Of the seven regular observers, only one (observer number 4) conducted sampling in different years (Table 3). This resulted in confounding of observer and year effects.

There were highly significant effects of transect on adult deer and fawns seen per

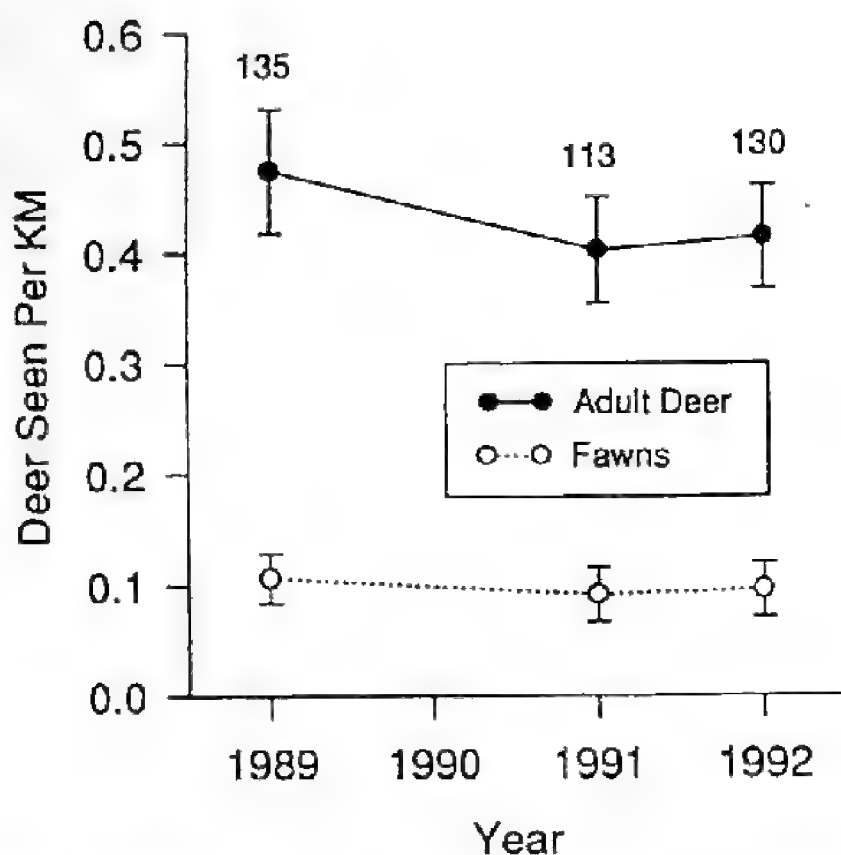


Figure 2. Mean number of adult deer and fawns seen per km of transect driven for each of the 3 years. Error bars are 95% confidence intervals, and sample sizes (total number of transects driven) are shown above each error bar.

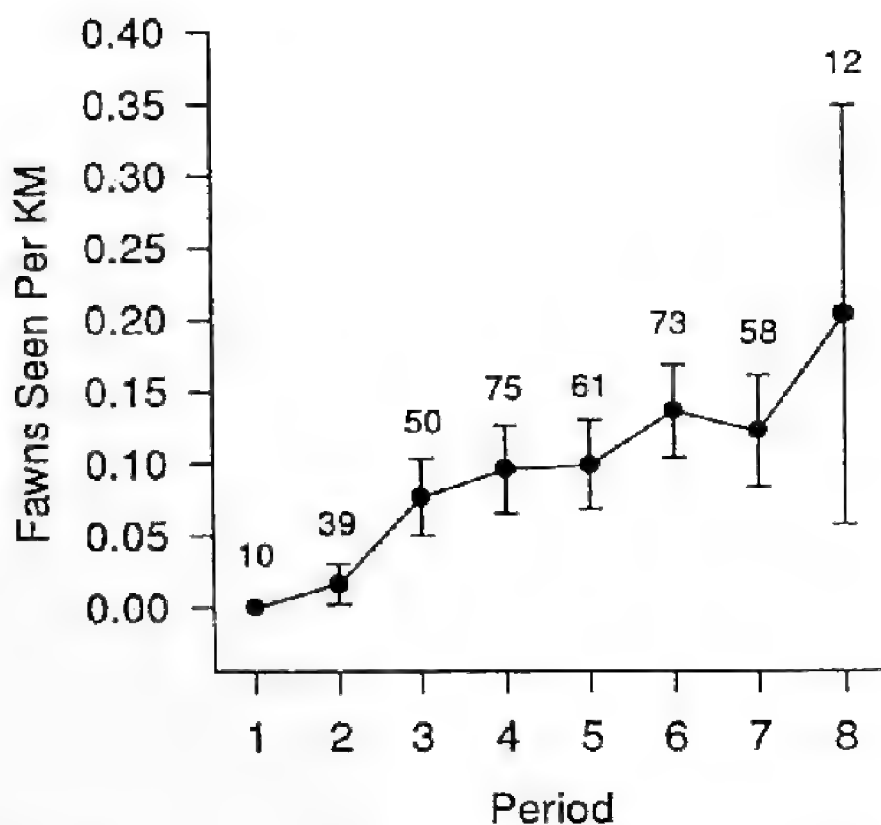


Figure 3. Mean number of fawns seen per km of transect driven by semi-monthly period from early June (period 1) through late September (period 8). Data from all 3 years combined. Error bars are 95% confidence intervals, and sample sizes (total number of transects driven) are shown above each error bar.

Table 3. Number of transects driven each year and mean and standard deviation of adult deer seen per km on each run by different observers. Observer codes 1-7 represent unique single observers, code 8 represents any two observers, and code 9 represents several miscellaneous single observers.

Observer Code	Transects/Year			Adult Deer Seen Per Km	
	1989	1991	1992	Mean	SD
1	33	0	0	0.433	0.371
2	33	0	0	0.558	0.369
3	24	0	0	0.378	0.234
4	0	54	59	0.383	0.223
5	0	53	0	0.393	0.286
6	0	0	52	0.492	0.320
7	0	0	18	0.344	0.272
8	18	6	0	0.520	0.326
9	27	0	1	0.468	0.277
All	135	113	130	0.432	0.293

km ($P < 0.01$) (Table 2, Fig. 4). There were significant year \times transect and period \times transect interactions for both adult deer and fawns seen per km ($P < 0.01$) (Table 2). Finally, moon phase as measured by number of days away from the nearest full moon had no significant effect on adult deer ($P = 0.31$) or fawns ($P = 0.77$) seen per km (Table 2).

Sex and Age Ratios

Of 1,757 adult deer seen during all 3 years, 88% were female. Of 1,622 groups of deer seen, few groups ($n = 51$) contained both adult males and adult females. Of the remaining 1,571 single-sex groups, only 82% consisted of adult females (compared to 88% of the population being female). We believe this pattern resulted from adult females occasionally being found with yearling males (fawns from the previous year, classified as adults in this study), while older adult males were more likely to form single-sex groups.

There were no significant effects of the main factors of year ($F_{2,326} = 0.10$), transect ($F_{5,326} = 1.67$), and period ($F_{7,326} = 0.94$) or the interaction of year \times transect ($F_{10,326} = 1.14$) on the buck:doe ratios (adult male deer per 100 adult females) for each transect run ($P > 0.10$). Yearly means were 16.2 (SD = 34.5), 15.7 (SD = 28.5), and 18.0 (SD = 39.8) bucks:100 does for 1989, 1991, and 1992, with an overall 3-year estimate of 16.7 (SD = 34.8) bucks:100 does. However, our sample sizes were small, ranging from nine to 24 groups of deer seen during any single transect-year combination, and it is unlikely we would have detected even a large change in the true ratio.

Transect ($F_{5,326} = 0.33$), and year \times transect interaction ($F_{10,326} = 1.54$) did not affect the number of fawns seen per 100 adult females ($P > 0.10$). There was a significant effect of year ($F_{2,326} = 6.16$, $P < 0.01$) and period ($F_{7,326} = 5.72$, $P < 0.01$), on fawns:100 does.

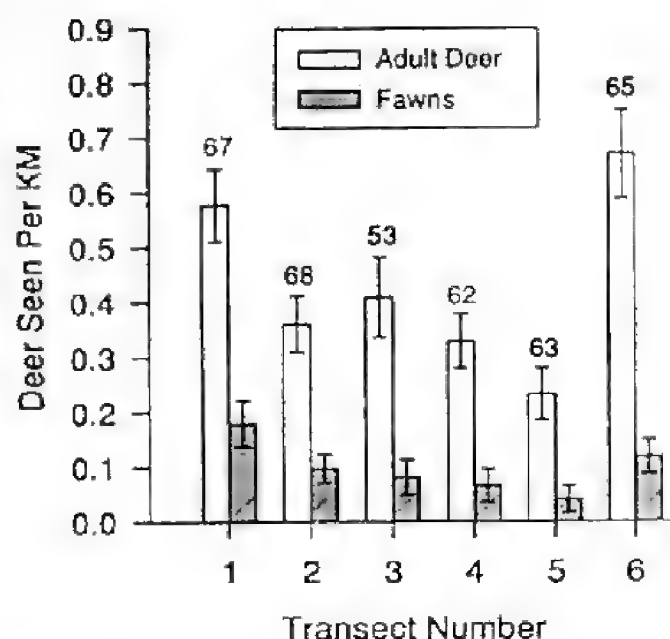


Figure. 4. Mean numbers of adult deer and fawns seen on each transect. Transect names are: 1 = Exchequer Meadow, 2 = Cabin Meadow, 3 = Big Fir, 4 = Ahart Meadow, 5 = Smith Meadow, and 6 = Hoffman Mountain. Data from all 3 years combined. Error bars are 95% confidence intervals, and sample sizes (total number of transects driven) are shown above each adult deer histogram.

Estimated fawn:doe ratios increased steadily from early June through September, and averaged 28.0 (SD=38.0) in 1989, 31.3 (SD=52.0) in 1991, and 38.0 (SD=74.8) in 1992.

Sample sizes for all transects (number of transect runs where at least one adult doe was seen) were the same for fawn:doe ratios as for buck:doe ratios (1989 = 127 runs, 1991 = 103 runs, and 1992 = 121 runs). This resulted in erratic ratios when examining transect-year combinations because of small sample sizes.

Estimates of Deer Density

Program DISTANCE chose four different models to portray frequency-distance data for the 18 transect-year combinations (Fig. 5). Once a model was chosen (based on clusters or groups of deer seen), DISTANCE tested to see if larger groups were more visible than smaller ones at longer distances. In only two cases, Cabin Meadow in 1989 and Exchequer Meadow in 1992, was there a significant ($P < 0.05$) size-bias in group visibility (Table 4). Therefore, the size-biased regression was used to estimate individual deer densities in those two cases, and the mean cluster size was used in the remaining instances (Table 4).

Fewer deer were seen in the first 18-m interval than in the second interval (19-36 m) in 12 of the 18 transect-year combinations (Fig. 5). However, there was no significant relationship between the percentage of standing deer and their distance away from the center of the transect (regressions for each transect run separately were all $P > 0.10$). We concluded that if evasive movement was occurring, it was slight. We further suggest that the observation of fewer deer adjacent to the transects resulted from the general tendency of deer to avoid roads (Rost and Bailey 1979).

Highest deer densities were seen on the Exchequer Meadow transect each year,

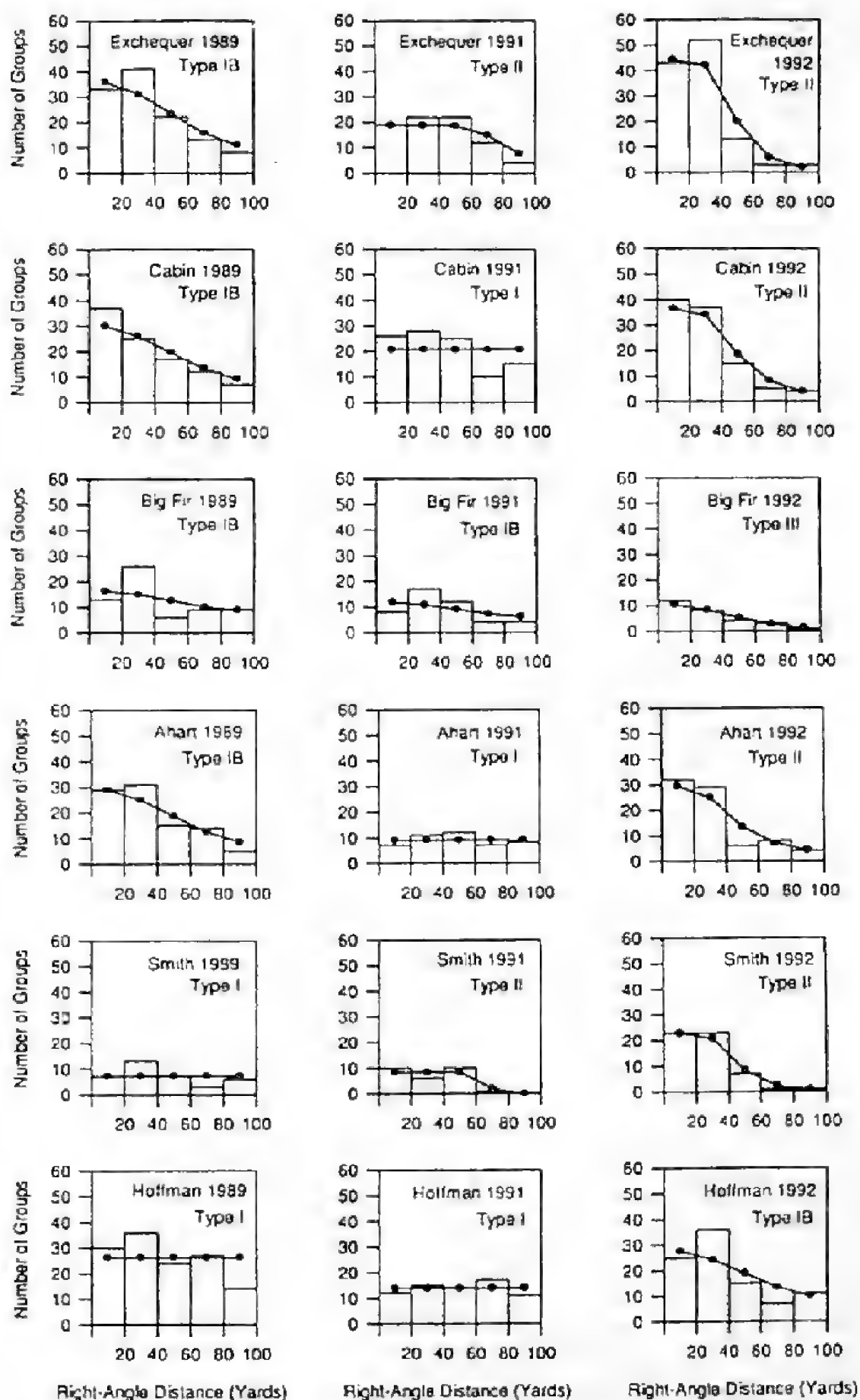


Figure 5. Detection functions fitted by Program DISTANCE. Vertical axes are numbers of clusters (groups of deer seen), horizontal axes are perpendicular distance intervals of 18, 37, 55, 73, and 91 meters. Detection curve types are: I = uniform, IB = uniform with first-order cosine adjustment, II = hazard rate, and III = half-normal.

Table 4. Estimates of adult deer densities derived from program DISTANCE. Degrees of freedom (df) determined according to Satterthwaite (1946).

Year and Transect	Adult Deer Per Square Km		
	df	Mean	(95% CI)
1989			
Exchequer Meadow	174	5.24	(4.13-6.65)
Cabin Meadow ¹	140	2.32	(1.79-3.00)
Big Fir	81	2.81	(1.96-4.05)
Ahart Meadow	131	3.76	(2.89-4.91)
Smith Meadow	35	1.04	(0.75-1.45)
Hoffman Mountain	130	4.04	(3.36-4.86)
All 1989	5	3.17	(2.01-5.02)
1991			
Exchequer Meadow	119	3.35	(2.53-4.44)
Cabin Meadow	103	2.40	(1.94-2.97)
Big Fir	58	2.50	(1.58-3.94)
Ahart Meadow	44	1.10	(0.81-1.49)
Smith Meadow	26	1.52	(1.01-2.30)
Hoffman Mountain	68	2.56	(1.95-3.36)
All 1991	5	2.20	(1.51-3.22)
1992			
Exchequer Meadow ¹	134	5.79	(4.58-7.33)
Cabin Meadow	142	2.90	(2.19-3.82)
Big Fir	41	4.39	(2.67-7.21)
Ahart Meadow	87	2.81	(1.98-3.98)
Smith Meadow	72	3.50	(2.48-4.93)
Hoffman Mountain	149	4.30	(3.28-5.64)
All 1992	5	3.71	(2.68-5.15)

¹ Size-biased cluster (group) estimate used to calculate deer density; mean cluster size used in all other cases (see text).

with the Hoffman Mountain transect exhibiting the second highest densities for 2 of the 3 years studied (Table 4). Mean density was lowest in 1991 (2.20 deer/km²) and highest in 1992 (3.71 deer/km²), but the broad confidence intervals overlapped (Table 4). Using deer densities as an index to change in population size suggested a different response in 1992 (Fig. 6) that was not shown by simple numbers of deer seen each year (Fig. 2). But in either case, we concluded that there was no significant change in total population size.

DISCUSSION

Current methods for estimating population size based on harvest of male deer in the North Kings herd suffer from unknown accuracy and precision, and they yield no

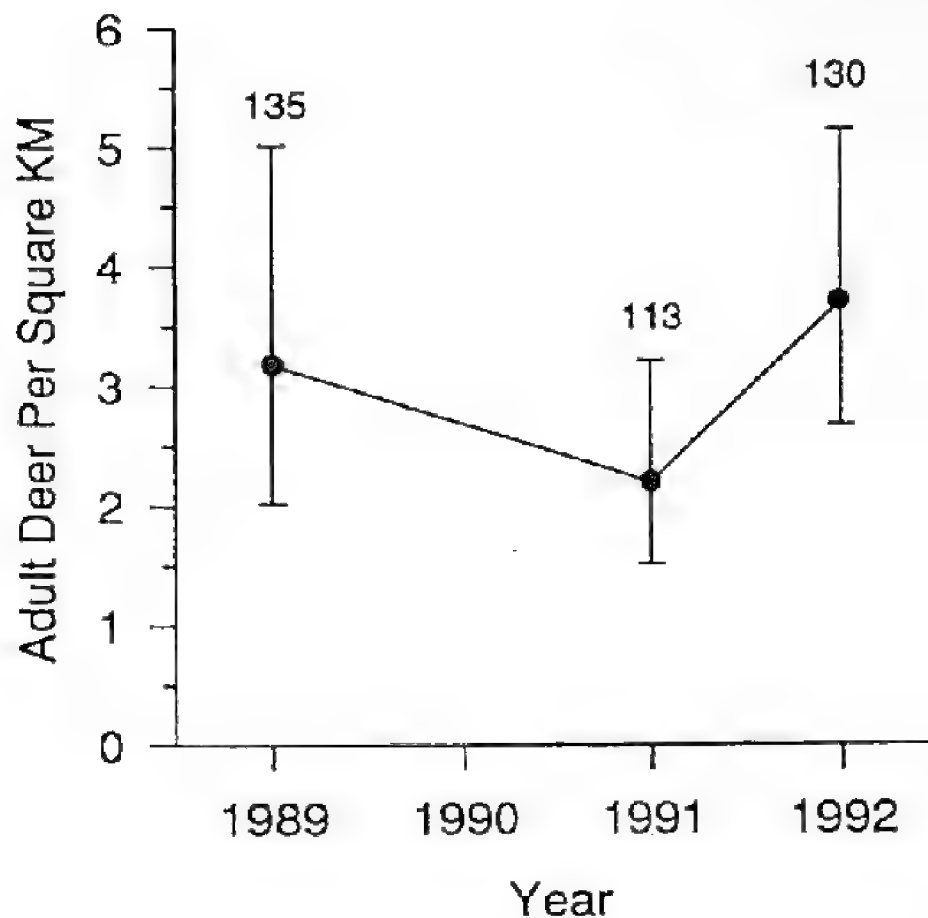


Figure. 6. Estimated deer densities for each of the 3 years. Error bars are asymmetrical 95% confidence intervals, and sample sizes (total number of transects driven) are shown above each error bar.

measure of sample variability. Our first objective was to determine whether numbers of deer seen during spotlight transects could be used as an index to changes in deer population size. As expected, we found that fawns were not seen very frequently on the transects until late in the summer. Deer fawns are usually not found with their dams continuously until they are ≥ 1 month of age. As a result, spotlight transects conducted during the summer months are not reliable in estimating numbers of fawns (McCullough 1982).

Numbers of adult deer seen differed between transects, suggesting the importance of using a representative sample of transects to cover the geographic area of interest. Transects could be allocated randomly or in a stratified random manner, but the results obtained will be applicable only to the area over which they are distributed.

Moon phase, measured as number of days away from the nearest full moon, did not affect the numbers of adult deer seen. If adult females feed less and rest more on nights with a full moon as previously reported (Kie et al. 1991), this behavioral pattern did not influence their probability of being observed. Although weather and environmental factors such as air temperature and precipitation can affect numbers of deer seen on spotlight transects (Progulske and Duerre 1964), conditions during our study were relatively constant during the months we were conducting counts.

Annual differences in numbers of deer seen can result from: (1) changes in deer population size between years, (2) variations resulting from factors not accounted for

as well as random sampling variation, and (3) using different observers each year with differing abilities to detect deer on the transects. Working with sex and age ratios in black-tailed deer, McCullough (1993) reported differences between years but ruled out observer effects because of intensive training and deer population effects because of lack of corroborative evidence about population changes.

Our results indicate that despite our attempts to train observers to an equal level of proficiency, people differ in their ability to see deer. We used different observers almost every year, with the exception of one person who conducted counts during 2 of the 3 study years. As a result, observer effects were confounded with yearly differences resulting from actual changes in deer population size and other factors. We also agree with McCullough (1993) that using spotlight count data to estimate deer herd sex and age ratios should be treated with caution.

Our second objective was to determine whether recording perpendicular distances could be used to estimate deer density based on line transect theory. We found that those estimates could be derived, but although they suggested a slight increase in total adult deer numbers in 1992 (Fig. 6) that was not revealed by numbers of deer seen per km of transect driven (Fig. 2), high variability and lack of statistical significance did not support that conclusion.

The third and final objective was to determine if estimates of adult deer density could be applied to estimating actual population size in the North Kings deer herd. We concluded that they could not. First, we did not know precisely how deer were distributed with respect to roads. Our analysis of standing versus bedded deer suggests that animals were not moving away from the center of the transect before they were detected, yet several of the transect-year combinations indicated fewer deer in the first transect interval (< 18 m) than expected (Fig. 5). This led us to conclude that deer were avoiding the area adjacent to the roads we used as transects. We do not know the nature or extent of that avoidance, nor how it varies as functions of road type, frequency of traffic, and other factors.

Secondly, four of our six transects were located on the western half of the summer range (Dinkey segment), although the two most eastern transects were located on the edge of the Crown segment. As a result, we believe that our data indicate trends in adult deer numbers on only part of the summer range used by the North Kings herd. However, we suggest that this is an acceptable limitation for purposes of deer herd management, because most of the harvest occurs on the more accessible Dinkey segment, and accurate knowledge about changes in deer numbers is more important for that portion of the herd.

The alternative to road-based transects are counts conducted on foot, a practice strongly recommended for many other species (Buckland 1994, Buckland et al. 1993). However, trying to count deer in the North Kings herd on foot, even during daylight, would almost certainly result in deer moving off the transect before being detected, thereby violating the primary assumption of transect analytical methods. Furthermore, such counts would be labor-intensive and prohibitively costly.

We have no basis in this study to recommend for or against the estimation of deer densities as an index to total population size over simply recording the numbers of deer

seen on transects. However, we are reluctant to disregard the utility of line transect methods. If habitat alteration that effects deer visibility was occurring, such as timber harvesting, then line transect methods using perpendicular distances should in theory be able to account for those alteration-induced changes in visibility.

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INVASION OF A THIRD ASIAN GOBY, *TRIDENTIGER BIFASCIATUS*, INTO CALIFORNIA

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The Sacramento-San Joaquin Estuary is a major international port and ballast water dumping by ships has been the source of numerous introductions of exotic invertebrates (Carlton et al. 1990) and several fishes (Carlton 1985), including the yellowfin goby, *Acanthogobius flavimanus*, and the chameleon goby, *Tridentiger trigonocephalus*, (Brittan et al. 1963). This note documents the establishment of a third exotic goby, *Tridentiger bifasciatus*.

Recently, Akihito and Sakamoto (1989) reinstated *T. bifasciatus* as a separate and valid species after over 50 years of synonymy with *T. trigonocephalus* (Tomiyaama 1936). Both *T. bifasciatus* and *T. trigonocephalus* are native to Asian estuaries and have very similar physical characteristics and color morphs. We have summarized (Table 1) details concerning distinguishing characteristics, adapted from Akihito and Sakamoto (1989). Additionally, *T. trigonocephalus* is primarily marine and is rarely found in salinities less than 22‰, whereas *T. bifasciatus* is commonly collected in fresh water and has not been collected in salinities above 22‰ (Akihito and Sakamoto 1989). However, salinity ranges of these species do overlap and in Japanese estuaries they are found sympatrically (K. Sakamoto, Biological Laboratory, Imperial Household, Japan, pers. commun.).

Tridentiger trigonocephalus has a history of rapid establishment in California. In 1960 two *T. trigonocephalus* were observed on a rock jetty in Los Angeles Harbor (Haaker 1979), one of which was collected. In 1962 a *T. trigonocephalus*, apparently representing a separate introduction, was collected from the Redwood City docks (Fig. 1) in South San Francisco Bay (California Academy of Sciences [CAS] 27011) and by 1964 this species was listed as a resident of the San Francisco Bay region (Ruth 1964). In light of the recent reevaluation by Akihito and Sakamoto (1989), we reexamined the 1962 San Francisco Bay specimen (CAS 27011), compared it to descriptions found in Steindachner (1881), Fowler (1972), and Akihito and Sakamoto (1989), as well as with other specimens of Asian origin housed at the CAS, and confirmed it to be *T. trigonocephalus*.

Until 1985, when fish thought to be chameleon gobies were collected in the lower

Table 1. Distinguishing characteristics of *T. trigonocephalus* and *T. bifasciatus* (adapted from Table 3 in Akihito and Sakamoto 1989).

<u><i>Tridentiger trigonocephalus</i></u>	<u><i>Tridentiger bifasciatus</i></u>
1) upper ray of pectoral fin free and usually covered with conical projections	1) upper ray of pectoral fin attached and smooth
2) large sensory canal pores in the the interorbital region of the head	2) small sensory canal pores in the interorbital region of head
3) white speckles on head large and do not extend to ventral surface	3) white speckles on head small and extend to ventral surface
4) dorsal and anal fins edged with white	4) dorsal and anal fins edged with orange

salinity waters of the upper Sacramento-San Joaquin Estuary, the chameleon goby was recorded only in the marine environments of the estuary. This upstream extension was believed to be the product of drought-related salinity encroachment into the upper estuary (Swift et al. 1993, Meng et al. 1994). Subsequently, however, otter trawl catch-per-unit-effort data from the California Department of Fish and Game seemed to indicate that the chameleon goby's distribution along the estuarine salinity gradient had changed from being restricted to high salinities (prior to 1985) to having peaks in saline and fresh waters (Fig. 2).

Based on Akihito and Sakamoto's (1989) criteria, we reexamined *Tridentiger* specimens collected from fresher water, previously identified as *T. trigonocephalus*, and found them to be *T. bifasciatus*. These specimens were collected in Suisun Marsh (Fig. 1) in 1985 (Peter B. Moyle, University of California at Davis, unpublished data) and at the John E. Skinner Delta Fish Protective Facility near Byron, Contra Costa County (Fig. 1), in 1987 (Raquel 1988). Now, after examining several hundred specimens from the estuary, we believe that all *Tridentiger* from the limnetic and low salinity regions of the estuary are *T. bifasciatus*. We have deposited voucher specimens (CAS 81588, 81592, and 82361) at the CAS.

By 1989, *T. bifasciatus* was the most abundant adult fish within Suisun Marsh (Meng et al. 1994) and the third most abundant larval fish collected in ichthyoplankton tows by the California Department of Water Resources (DWR) in the southern Delta (IESP 1990). In 1990 it was the most abundant larva collected by the CDWR (IESP 1991) and had been transported via the California Aqueduct approximately 513 km south to Pyramid Reservoir (Fig. 1; Swift et al. 1993). In 1992 it was collected downstream of that reservoir in Piru Creek (Fig. 1; Swift et al. 1993) but has yet to be collected from Piru Lake farther downstream or downstream of Piru Lake (M. Guisti, California Department of Fish and Game, pers. commun.). The specimens within and below Pyramid Reservoir were originally identified as *T. trigonocephalus*, but in 1994 they were inspected by J. Seigel, Natural History Museum of Los Angeles County, who determined that they

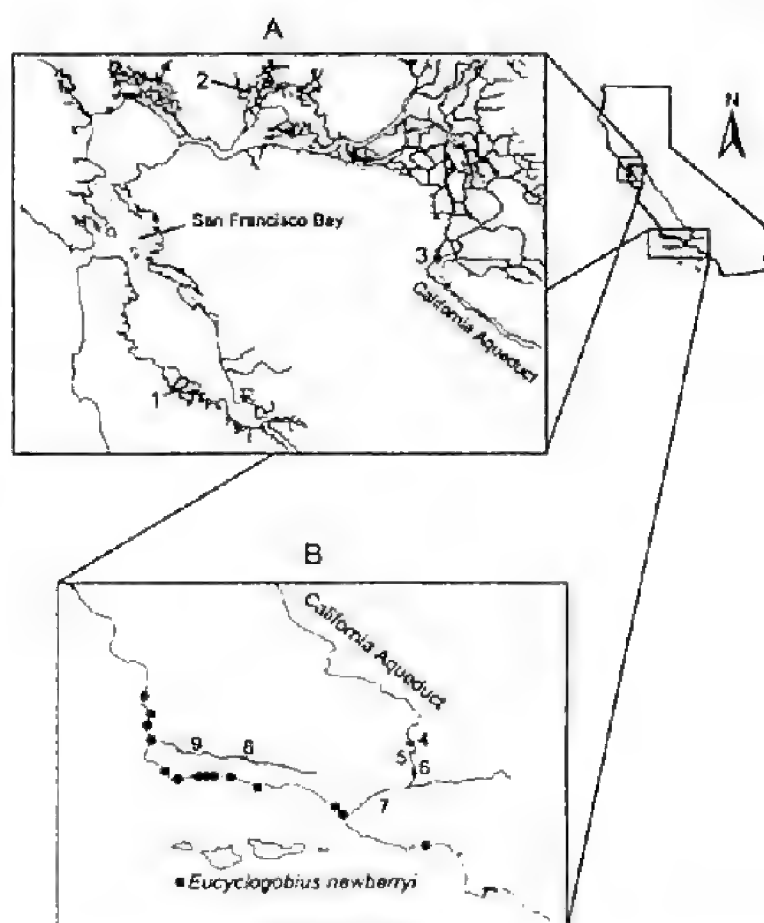


Figure 1. Spread of *Tridentiger* spp. in California. A. Sacramento-San Joaquin Estuary: 1. *T. trigonocephalus* collected in 1962 at the Redwood City municipal piers; 2. a *T. bifasciatus* collected in 1985 in Suisun Marsh; 3. a *T. bifasciatus* collected in 1987 at the John E. Skinner Delta Fish Protective Facility. B. Southern California drainages: 4. *T. bifasciatus* collected in 1990 in Pyramid Reservoir; 5. *T. bifasciatus* collected in Piru Creek in 1992. No *Tridentiger* spp. have been found in Piru Lake (6), the Santa Clara River (7), Lake Cachuma (8), or the Santa Ynez River (9). *Eucyclogobius newberryi* locations (Swift et al. 1993) marked for comparison.

were *T. bifasciatus*.

Given the late arrival of *T. bifasciatus* to the estuary, we believe that Wang's (1986) early life history accounts refer only to *T. trigonocephalus*. Like the chameleon goby, *T. bifasciatus* prefers habitats with structurally complex substrates (Akihito and Sakamoto 1989) and, where distributions overlap, both may spawn in the same areas (K. Sakamoto, Biological Laboratory, Imperial Household, Japan, pers. commun.). Based on collections of *Tridentiger* spp. larvae within the freshwater portions of the upper Estuary, spawning of *T. bifasciatus* occurs from April through September (IESP 1994).

Mature *T. bifasciatus*, held at the University of California at Davis, readily spawn in 25-mm diameter polyvinylchloride tubes in water of less than 5‰ salinity at 20°C. At this temperature larvae hatch in about 9 days. Males guard the eggs and often spawn with several females, which are partial spawners. In Suisun Marsh, *T. bifasciatus* feeds primarily on benthic invertebrates such as amphipods and mysid shrimp (Peter B. Moyle, University of California, Davis, unpublished data). Dietary and habitat preferences of *T. bifasciatus* potentially place it in direct competition with the federally

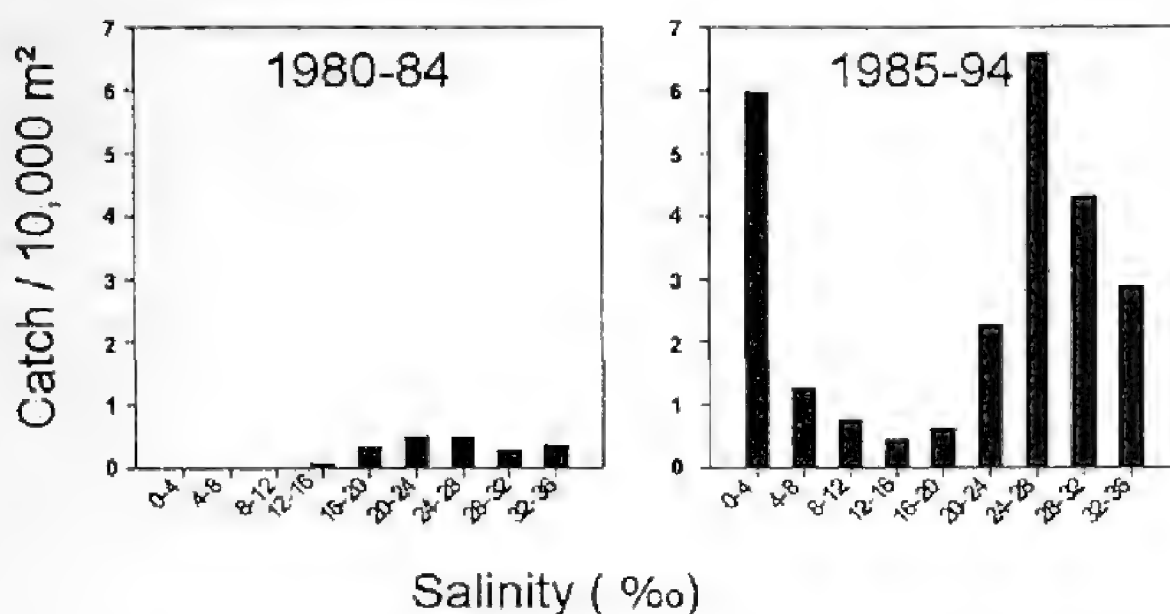


Figure 2. Salinity distribution of *Tridentiger* spp. collected in the Sacramento-San Joaquin Estuary. Catch-per-unit-effort and salinity data were collected monthly between 1980 and 1994 at fixed otter trawl sampling stations throughout the estuary by the California Department of Fish and Game.

endangered tidewater goby, *Eucyclogobius newberryi* (Brewer et al. 1994). This hypothesis was supported by laboratory studies demonstrating that *T. bifasciatus* will prey upon, disrupt spawning of, and reduce feeding of tidewater gobies (Swenson and Matern, in prep.). Although these species appear to be allopatric, the potential for interaction may be realized soon, either via "natural" range extension by *T. bifasciatus* or "assisted" range extension via the State Water Project System. Unless adequate precautions are taken, this scenario may occur when water from the California Aqueduct is diverted into Lake Cachuma (Figure 1) in southern California (SAIC 1993). Water from this reservoir flows into the Santa Ynez River (Figure 1), and could deliver *T. bifasciatus* larvae and adults to the coastal brackish water habitats of *E. newberryi*. It is therefore of utmost importance that, as planned (SAIC 1993), diverted water is treated before it reaches Lake Cachuma. The tidewater goby populations in the lower Santa Clara River (Figure 1) face an even greater threat since *T. bifasciatus* is established upstream in Piru Creek. Swift et al. (1993) predict downstream movement throughout this drainage by *T. bifasciatus*, an invasion which may have been accelerated by the severe winter floods of 1995.

Although this is the first record of *T. bifasciatus* outside its native range, it may also be established in Australia. Hoese (1973) and Friese (1973) reported the occurrence of *T. trigonocephalus* in Sydney Harbor and the species was subsequently reported as established there (Pollard and Hutchings 1990). Given the physical similarities between these two gobies and their recent taxonomic separation, *T. bifasciatus* may be an undetected resident of Australia as it was for several years in California, especially if the *Tridentiger* populations occur in low salinity waters.

The common name for *T. trigonocephalus* has been established by the American Fisheries Society as the chameleon goby (Robins et al. 1980). There is no official common name for *T. bifasciatus*. We propose slightly modifying and adopting this

fish's new Japanese name, "shimofuri shimahaze" (Akihito and Sakamoto 1989), as its common name. "Shimofuri," which lacks a direct English equivalent, refers to fat-marbled beef and aptly describes the pattern of white spots on the head of *T. bifasciatus*. "Shimahaze" means "striped goby" and will be dropped to avoid confusion and redundancy. We therefore propose that *T. bifasciatus* be known as the shimofuri goby.

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FEEDING ON EUPHAUSIIDS BY *OCTOPUS RUBESCENS*

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While conducting remotely operated vehicle (ROV) video transects for fish community studies, we observed *Octopus rubescens* feeding on unidentified euphausiids. *Octopus rubescens* is a small octopus common along the Pacific coast of the United States from Alaska to Baja California found at depths from the low intertidal to about 200 m (Hochberg and Fields 1980). The little information on *O. rubescens* feeding in the wild indicates that they prefer small crabs and hermit crabs, and feed mainly on crustaceans, mollusks, and fishes (Dorsey 1976, Hochberg and Fields 1980). We observed *O. rubescens* (approximately 75 mm mantle length) feeding on euphausiids, a unique prey item, and, due to this unusual encounter, we noted the capture methods and compared the octopus density in areas with and without euphausiid swarms.

Cruises were conducted aboard the Monterey Bay Aquarium Research Institute's R/V *Point Lobos* using the ROV, the *Ventana*. The transects were conducted on mud-sand bottoms at 200 m off Santa Cruz, California, on October 1 and 17, 1991. The ROV travelled at approximately 1.8 km/hr and stopped only occasionally for species identification and maintenance. The ROV was equipped with a three chip video camera and four 400-watt sodium-scandium lights.

The euphausiids could not be identified to species. The size of the euphausiids was approximately 10 mm carapace length, and this was fairly homogeneous throughout all swarms. Euphausiid swarm densities were in the range of hundreds per cubic meter. The euphausiid swarms appeared to occur naturally and were not a result of attraction to the ROV lights. We encountered the euphausiid swarms on two separate days over a 16-day period, and these were only in the same locations. This spatial consistency over 16 days indicates that the swarms were persistent in this area and not a result of

the ROV lights. Also, we came upon octopuses whose webs were filled with euphausiids. Since the ROV was constantly moving, the octopuses must have been feeding on euphausiids before the ROV was in the area.

Octopus rubescens was observed to feed on euphausiids using three different capture methods. The most frequently observed capture method began with the octopus resting on the bottom, then "pouncing" toward the euphausiid and capturing it in its webbing. Once a euphausiid was located (most probably visually), the octopus would slowly crawl toward it and, when close enough (typically closer than twice the mantle length of the octopus), the octopus would cease forward movement while extending one or two of the closest arms. It then would raise up on the remaining arms and throw its body up and over the euphausiid, then descend over it, encircling the euphausiid in its web. Frequently, the euphausiids were so close together that the octopus would make repeated attacks without having to crawl first. This is similar to the attack method described by Maldonado (1964), Warren et al. (1974), and Hanlon and Wolterding (1989).

Octopus rubescens had a distinctive change in body pattern during its attack. Before any attack posture, the octopus had a dark reddish-brown pattern. An instant before the pounce, the octopus would change its body pattern to white or gray. Upon landing, the octopus would change back to the reddish brown pattern, with a darker, more intense brown. The change in body pattern during attack that we observed differed from that described by Warren et al. (1974) for this species. They observed that the octopus became transparent enough to see internal organs at the moment of landing on the prey. Warren et al. (1974) believed that these body pattern changes were due to changes in locomotor activity during attacks.

In the second capture method, *O. rubescens* was suspended off bottom, typically more than 1 m. The body was upright and the arms were spread radially. The animal would slowly sink until one of the arms encountered a euphausiid. Upon contact, some of the arms would grasp the euphausiid and the octopus would descend to the bottom and consume the euphausiid. We only observed this behavior from a distance when the octopus was already suspended in the water. This behavior also has been observed for an unidentified octopus feeding on zooplankton (Clarke et al. 1967).

Occasionally, an octopus tried to capture another euphausiid after its web appeared full. While remaining stationary, the octopus would extend one arm outward and attempt to grasp an euphausiid. This method was infrequently successful and is similar to the "side arm attack" described by Hanlon and Wolterding (1989).

Densities of *O. rubescens* were not significantly different between areas with and without euphausiid swarms (mean abundance = 1,796 and 1,684 octopuses/ha); however, the intensity of feeding behavior varied. As might be expected, in areas with euphausiid swarms, 94 octopuses were observed feeding compared to only 15 in the areas without euphausiid swarms. This suggests that octopuses were not drawn to areas specifically to feed on euphausiids. Rather, euphausiids are probably a patchy and sporadic resource near bottom.

Octopus feeding on euphausiids is unique. The only reference is to laboratory feeding on frozen euphausiids (Marliave 1981). However, pelagic prey has been found

in octopus diets, including mysids, large copepods, and ostracods (Boucher-Rodoni et al. 1987; Nixon 1985, 1987; and Boletzky and Hanlon 1983). Many of these pelagic items were eaten by juveniles. The feeding on pelagic prey by benthic adult octopus has rarely been reported. With the increase of visual observations below SCUBA depths, the knowledge of octopus diets will continue to expand.

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FIRST OCCURRENCE OF THE YELLOW BULLHEAD, *AMEIURUS NATALIS*, IN THE LOWER COLORADO RIVER, BAJA CALIFORNIA, MEXICO

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On May 28 and August 27, 1994, seven specimens (standard length 174-225 mm and weight 83-144 g) of yellow bullhead, *Ameiurus natalis*, were captured with 25-m experimental gill nets in the lower Colorado River, approximately 100 m upstream from its confluence with the Río Hardy in Mexicali County, Baja California, Mexico (32° 06' N and 115° 14' W). This report represents the first record of this species in the lower Colorado River of Mexico.

The yellow bullhead is native to the eastern and central United States (Glodek 1980), including the Rio Grande (Río Bravo) basin (Page and Burr 1991). The typical habitat for this species is clear, warm waters with permanent flows and rocky bottoms (Minckley 1973). The yellow bullhead has been widely introduced outside its native range (Page and Burr 1991). This species was first introduced into California in 1874 (Curtis 1949) but it is still considered to be rare in southern California (McGinnis 1984, Swift et al. 1993). In that region, its scarcity plus morphological similarity to the brown bullhead, *Ameiurus nebulosus*, has resulted in a distribution that is not well known (Moyle 1976). The exotic distribution of the yellow bullhead in México was previously reported by Contreras (1987) in the Rio Grande at Chihuahua (Ciudad Juárez and Isleta). Minckley (1973) noted that the yellow bullhead is widespread but rare in collections from Arizona, including the Colorado River.

The collected specimens of yellow bullhead were identified by the following diagnostic characteristics (cf. Minckley 1973, Moyle 1976, Page and Burr 1991): yellow chin barbels; long anal fin, nearly straight in outline; 24-27 anal rays, rays at front only slightly longer than rear rays; eight large sawlike teeth on rear of pectoral spine; body yellow-olive with white belly. The number of fin rays of seven specimens examined varies as follows: dorsal, 6 to 7 (mean 6.14); anal, 25 to 26 (mean 25.14); pectorals, 8 to 9 (mean 8.14); pelvics, 8; and caudal, 20 to 21 (mean 20.43).

The occurrence of the yellow bullhead in the collecting site may be an indication of a recent downstream dispersal in the Colorado River from Arizona, or possibly its occurrence has been overlooked due to the lack of ichthyological studies in this region of Mexico. I recommend that the distribution of the yellow bullhead and other exotic species in the lower Colorado River of Baja California and Sonora be monitored in order to evaluate their impact on native fish populations.

The specimens are deposited in the Fish Collection, Laboratorio de Vertebrados,

Facultad de Ciencias, Universidad Autónoma de Baja California, Ensenada, Mexico (specimens UABC-0091 and UABC-0093).

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PREHISTORIC FISH REMAINS, INCLUDING THICKTAIL CHUB, FROM THE PAJARO RIVER SYSTEM

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The Pajaro River system in Central California now supports 11 native fishes as well as a variety of exotic fish species. Two additional native species were historically present but are now locally extinct (Smith 1982). Analysis of recently-excavated prehistoric fish remains from the drainage demonstrates the former presence not only of the two extirpated fishes, but of an additional extinct species as well.

Archaeological site CA-SCL-119/SBN-24/H is a prehistoric midden located near San Felipe Lake at the confluence of Pacheco Creek and the Pajaro River. Test excavations in 1991 produced a series of radiocarbon determinations that date the deposit at ca. AD 600-1300 (Hildebrandt and Mikkelsen 1992). A total of 26 m³ of midden was processed through 84-mm or 42-mm mesh screens, and all recovered vertebrate faunal material was saved. Fish remains were investigated by the author.

Material examined included 986 elements. Those identified to species included 511 elements, representing six fishes (Table 1). The majority of the specifically identified remains are from one now-extirpated form, the Sacramento perch. Also well-represented was the thicktail chub, a species whose former presence in the Pajaro system has been uncertain. Additionally present were Sacramento sucker, hitch, Sacramento blackfish, and another now-extirpated species, the tule perch.

The small size of the archaeological fauna limits its interpretive value, and its composition is undoubtedly influenced by the large-mesh screens used in sampling (Gobalet 1989). Thus the absence here of sculpins, sticklebacks, and small minnows does not necessarily indicate their absence from the local prehistoric fishery. The same factor may account for the paucity of tule perch remains in this sample.

Additionally, relative abundance of the elements of different species is influenced by diagnostic factors. The high number of Sacramento perch elements identified, in particular, reflects the osteological distinctiveness of this species in comparison to the other fishes present. Calculation of minimum number of individuals (based on the most frequently occurring single element) produces smaller sample sizes, but provides a more reliable representation of the original deposition of different species in the midden.

Given these caveats, the fauna is informative. Of the species present, all except Sacramento sucker (which is but modestly represented) characteristically inhabit lentic environments. Such a predominance of slow-water forms is to be expected from a lakeshore fishery. The fauna clearly reflects the low-gradient blackfish association described by Smith (1982) and provides evidence of that association pre-dating the introduction of exotic species.

TABLE 1. Fish Remains from Site CA-SCL-119/SBN-24/H.

Common Name	Scientific Name	Number of Elements	Minimum Number of Individuals
Sacramento sucker	<i>Catostomus occidentalis</i>	15	5
Thicktail chub	<i>Gila crassicauda</i>	64	23
Hitch	<i>Lavinia exilicauda</i>	36	16
Sacramento blackfish	<i>Orthodon microlepidotus</i>	45	12
Minnows	Cyprinidae	206	-
Suckers or minnows	Cypriniformes	269	-
Sacramento perch	<i>Archoplites interruptus</i>	344	13
Tule perch	<i>Hysterocarpus traskii</i>	7	2
TOTAL		986	71

The fishes endemic to the Pajaro undoubtedly originated in the neighboring Sacramento-San Joaquin River system. An important member of the Sacramento-San Joaquin fauna, prior to its extinction in this century, was the thicktail chub (Miller 1963, Schulz 1979). The status of this species in the Pajaro River system and the adjacent Salinas River system has been uncertain.

A list (with proveniences) of all known thicktail chub specimens includes only two possible records from these drainages: one from "Salinas R." in 1923, the other from "Soap Lake, San Benito Co." in 1916 (Miller 1963). The Salinas River record has long been questioned (Hubbs 1947). Recent analysis of archaeological fish remains from Elkhorn Slough at the mouth of the Salinas River, however, has demonstrated the prehistoric presence of the species (Gobalet 1990, 1993).

In regard to the Soap Lake record, Gobalet (1990) notes that this lake has proven difficult to locate. In fact, Soap Lake is a local term for San Felipe Lake, the site of the present study. Located on the border of San Benito and Santa Clara counties, this lake was the location of an early 19th-century soap factory, and the resulting name is well-established in local historical sources (Laffey 1992). The present study documents the long-term presence of the thicktail chub at this locality and suggests that it was an important element of the prehistoric fishery of the Pajaro River system. The causes of its extirpation remain to be determined.

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OBSERVATIONS ON RECRUITMENT IN CURL-LEAF MOUNTAIN-MAHOGANY AS A RESULT OF SELECTIVE PRUNING

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Curl-leaf mountain-mahogany, *Cercocarpus ledifolius*, (mahogany) is an important part of the fall diet for Rocky Mountain mule deer, *Odocoileus hemionus*, in northeastern California (Leach 1956). Protein ratios in the stems and leaves are higher throughout the year than in many other shrub species (Plummer 1969) and stands of mahogany provide valuable cover. However, mahogany stands tend to decline in value to deer as they age and grow out of reach of animals or become decadent and decline in productivity. Mahogany is decadent on many sites in northeastern California, where little natural regeneration occurs despite periodically abundant seed crops (F. Hall, California Department of Fish and Game, pers. comm.). Efforts to improve browse availability and productivity are costly and often unsuccessful (Plummer 1974, Austin and Urness 1980, Schultz et al. 1990). Fire, herbicides, and mechanical manipulation are the methods most often used to improve browse species. Of these methods, few have been tried in dense stands of mahogany. Attempts to establish this species by direct seeding have failed (Liagos and Nord 1961).

I report on pruning of mahogany conducted each September from 1991-1993 on the Five-Dot Avila Ranch in Lassen County, California. The mahogany stands occurred in small patches, primarily on north- and west-facing slopes. Annual precipitation in the area averages 38 cm, mostly as winter snow. Summer thunderstorms provide about one-fourth of the annual precipitation. In 1991-92, the area received less than normal rainfall due to drought conditions. The rocky soils of the area are generally low in fertility, shallow, and poorly developed (Natural Resources Conservation Service, pers. comm.).

During fall, 70-75 mahogany trees showing basal or "sucker" growth were selected from several dense stands and pruned. Trees were checked weekly to determine seed ripeness and were pruned when the seeds were ripe, but before they dropped from the tree. One relatively large limb was cut from each tree and left on the ground. Germination and recruitment under and around the pruned limbs during the subsequent growing seasons were recorded.

Although seed quantity, rate of germination, and seedling vigor were not measured, seedling emergence appeared to be greater under and near the dead limbs during the 1st year following the treatment. Seedlings were not in small bunches as in rodent caches, but were irregularly distributed. Fewer seedlings were present in adjacent areas surrounding the treated tree and near untreated trees. Many seedlings had shallow root systems that barely penetrated the duff layer into the soil below. By the end of the second growing season, most of the seedlings had died. However, seedlings surviving

into the 2nd year appeared more abundant near felled limbs than in untreated areas. Most of these seedlings appeared to be recruited with little additional mortality. Observations from the third growing season were similar to those from the second season. Additionally, the number of new seedlings around previously pruned trees compared to unpruned trees appeared to increase. Similarly, Thompson (1970) found that a larger crop of mahogany seed was produced following top pruning, resulting in an increased number of seedlings the following season.

It is unclear what factors, related to pruning, influence germination and recruitment of mahogany. Limb pruning may open the canopy of dense stands sufficiently to allow increased light, heat, and/or moisture. Schultz et al. (1990) indicated that abundant mahogany reproduction occurred primarily where canopy closure was low. Downed limbs may hold snowfall longer, allowing for increased moisture penetration. Brotherson et al. (1984) reported that moisture conditions, and factors affecting moisture conditions, were significant in the development of mountain-mahogany communities. Additionally, birch-leaf mountain-mahogany, *Cercocarpus betuloides*, has been shown to exhibit less moisture tension after pruning (Campbell and Pase 1972), thereby increasing soil moisture levels. Moisture stress significantly decreased both the rate and final amount of germination and survival in true mountain-mahogany, *C. montanus* (Piatt 1976).

Protection from herbivory afforded by downed limbs may also increase recruitment. Scheldt and Tisdale (1970) reported that browsing of mahogany was the cause of poor stand recruitment and protected seedlings growing under slash piles exhibited significant new leader growth. However, in my assessment, germination of seedlings and recruitment of young mahogany appeared to be high around downed limbs as well as within them.

Plant communities are the product of biological, physical, and climatic influences. Effective management of curl-leaf mountain-mahogany requires knowledge of these influences on browse plants. Short of experimentation, observation and hands-on manipulation such as described here can help increase our understanding and knowledge of this plant species. Selective fall pruning of mahogany appeared to improve germination and recruitment of young plants dense stands. This suggests a potential for management of mahogany in selected areas. Additional research is needed to determine how pruning specifically affects germination and recruitment, and to develop pruning methods that can successfully treat large areas with less labor.

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BOOK REVIEW

WEBS AND SCALES, PHYSICAL AND ECOLOGICAL PROCESS IN MARINE FISH RECRUITMENT by Michael M. Mullin. 1993. University of Washington Press, Seattle and London. 135 p. \$25.00 hard cover, \$19.00 paperback.

This is the fourth book in the Washington Sea Grant monograph series. The series is intended to advance current, critical thinking on the study of fish recruitment as related to oceanography and better predict sustainable fisheries catch and to understand effects of climatic changes on marine organisms. Professor Mullin has achieved these goals in his volume which is based on lectures at the University of Washington and at Scripps Institution of Oceanography.

He discusses variability in marine, pelagic populations and communities by examining food "webs" in plankton as related to "scales" in time and space with an emphasis on the ecology of larval fish. He uses examples drawn from many research facets and disciplines studying biological variability in the ocean and relies on published research and copyrighted materials for an in-depth review of the topic, including numerous uses of data from the California Cooperative Oceanic Fisheries Investigation (CalCOFI). The book is written for those experienced in the terminology of ecology, fisheries, and biological and physical oceanography and is recommended for those interested in natural population variability relative to climatic variability.

The text is replete with references that offer significant pathways for further investigations into areas of interest reviewed or developed in this book. Throughout the book, he uses appropriate figures and illustrations to further enhance and explain concepts presented.

Professor Mullin has presented material that is logically organized to discuss temporal and spatial concepts of physical and chemical processes that may affect primary production and distribution of plankton. He further examines the ecological relationship of these horizontal micro- and mesoscales between phytoplankton and zooplankton. He reviews concepts of larval fish recruitment to adult populations on interannual and interdecadal time scales and suggests relevance to anchovy and sardine recruitment.

This book is a valuable and worthwhile addition to the Sea Grant monograph series on fishery recruitment and oceanography and additionally valuable to ecological literature in general. I recommend it to those exploring potential links and possible predictive value of atmospheric forcing and its effects on abundance and biomass at several trophic levels. For those following the monograph series, a fifth book by Dr. Andrew Bakun, FAO, is expected shortly from another publisher. Details are available from the Sea Grant office.

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